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PN W09954500 A2.
XX
XX PD 28 OCT 1999.
XX
XX PF 21-APR-1999; 99W0-IB00822.
XX
XX PR 21-APR-1998; 98US-0082614.
XX
XX PR 23-NOV-1998; 98US-0109732.
XX
XX PA (GEST ) GENSET.
XX
XX PI Cohen D, Blumentfeld M, Chumakov I;
XX
XX WP1; 2000-013267/01.
XX
XX PT Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX PS Claim 9; Page 2687; 2745pp; English.
XX
XX CC AA265654 to AA269578 represented human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA269579 to AA277440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses. They can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterization of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX N.B. The SEQ ID NOS 2862, 2912, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX SQ Sequence 21 BP; 14 A; 0 C; 7 G; 1 I; 0 other;

Alignment Scores:
Pred. No.: 75.7 Length: 21
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-070-16 (1-5) x AA277167 (1-21)

QY 1 GluAqGluLysGlu 5
Db 2 GAGAGAGAAAAGAG 16

RESULT 2
AA270346
ID AA270346 standard; DNA: 22 BP.
AC
XX
XX DI 16-JAN-1998 (first entry)
XX
XX DE Heterogeneous nuclear ribonucleoprotein (hnRNP) gene probe.
XX
XX KW Epithelial protein; heterogeneous nuclear ribonucleoprotein;
XX 70 kDa antigen; hnRNP-A2; hnRNP-B1; lung cancer; liver cancer;
XX renal cancer; prostate cancer; melanoma; head cancer;
XX neck cancer; myeloid; marked; carcinoma; genes; diagnosis; human;
XX probe; ss.
XX
XX OS Synthetic.
XX
XX PN W09712975-A1.
XX
XX PI Mulshine JL, Tockman MS;
XX
XX WP1; 1998-240016/21.

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PD 10-APR-1997.
XX
XX PF 02-OCT-1996; 96W0-US15825.
XX
XX PR 02-OCT-1996; 96US-0725027.
XX
XX PR 02-OCT-1996; 96US-0538711.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Mulshine JL, Tockman MS;
XX
XX DR WP1; 1997-226219/20.
XX
XX PT A new purified protein from epithelial cells is expressed in high
XX amounts in cancer and precursor cells; used as a marker for
XX diagnosis and treatment of cancer.
XX
XX PS Example 1; Page 34; 171pp; English.
XX
XX CC This antisense oligonucleotide can be used as a probe in Southern
XX blot analysis of heterogeneous nuclear ribonucleoprotein (hnRNP)
XX sequences. An epithelial protein (see AA26546-51) that shows
XX sequence homology to hnRNP A2/B1 is an early detection marker for
XX cancer, especially lung cancer.
XX
XX SQ Sequence 22 BP; 10 A; 3 C; 7 G; 2 T; 0 other;

Alignment Scores:
Pred. No.: 79.5 Length: 22
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-856-070-16 (1-5) x AA190346 (1-22)

QY 1 GluAqGluLysGlu 5
Db 1 GAGAGAGAAAAGGA 15

RESULT 3
AAV07133
ID AAV07133 standard; cDNA: 22 BP.
AC
XX
XX DI 09-SEP-1998 (first entry)
XX
XX DE Nucleotide sequence of an antisense oligonucleotide.
XX
XX KW Ribonucleotide protein; hnRNP2; human epithelial peptide; marker;
XX cancer; probe; hybridisation; primer; amplification; lung; liver;
XX kidney; breast; prostate, melanoma, myeloma; antibody; PCR; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN W09814469-A2.
XX
XX DI 09-APR-1998.
XX
XX PF 02-OCT-1997; 97W0-US17714.
XX
XX PR 02-OCT-1996; 96US 0725027.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Mulshine JL, Tockman MS;
XX
XX DR WP1; 1998-240016/21.

```

XX New isolated epithelial protein as early marker of cancer : useful
 PT in computer-assisted methods of diagnosis based on discriminant
 PT analysis of optical images of cells
 XX
 PS Disclosure: page 35; 159; English.
 XX
 CC This is the nucleotide sequence of an antisense oligonucleotide used
 CC in the method of the invention. Probes and primers that hybridize to
 CC or amplify these peptides are used to diagnose precancerous states,
 CC e.g. of lung, liver, kidney, breast, prostate, head or neck, melanoma
 CC or myeloma, or to determine susceptibility to these conditions and for
 CC monitoring treatment. Precancer is also indicated by detecting
 CC post-translational modification of the epithelial peptide which is a
 CC marker of epithelial cell transformation. Antibodies are potentially
 CC useful for diagnosis and treatment of cancer.
 XX
 SQ Sequence 22 nt; 3 A; 3 C; 7 G; 2 T; 0 other;
 Alignment Scores:
 Pred. No.: 79.5 Length: 22
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0
 US-09-856-070-16 (1 5) x AAG37133 (1-23)
 QY 1 GluArgGluysGlu 5
 DB 1 GACAGAGAAAGCAA 15
 RESULT 4
 AAC89363/c
 ID AAC89363 standard; DNA: 22 BP.
 XX
 AC AAC89363;
 XX
 DT 24-SEP-1999 (first entry)
 DE Chromosomal binding site for p53 protein (Seq ID No: 5 of US5936079)
 XX
 KW Cell growth inhibition, chromosomal binding site, p53 protein;
 KW cellular replication; cancer; ss
 XX
 OS Synthetic.
 XX
 PN US5936079-A.
 XX
 PD 10-AUG-1999.
 XX
 PF 15-AUG-1994; 94US-0291011.
 XX
 PR 01-MAY-1992; 92US-0879618.
 PR 04-AUG-1992; 92US-0863661.
 PR 15-AUG-1994; 94US-0291011.
 XX
 PA (ALTO-) ALTON OCHSNER MEDICAL FOUND.
 XX
 PI Cook J, Re R;
 XX
 DR WPI; 1999-457628/38.
 XX
 PT New oligonucleotide useful for treating and preventing cancer;
 XX
 PS Claim 1; Column 12; 12pp; English.
 XX
 CC The invention provides methods for inhibiting cell growth by providing a
 CC growing cell with an oligonucleotide capable of binding to a chromosomal
 CC binding site for p53 protein. Sequences AAX89362, AAX89363 and AAX89365
 CC represent oligonucleotides that are derived from the sequence AAX89355.
 CC The oligonucleotides are used for inhibiting mammalian cellular

CC replication and the treatment and prevention of cancer in a human. The
 CC oligonucleotides can be used in vitro to inhibit the growth of cultured
 CC mammalian cells e.g. human, monkey, mouse, rat and hamster cells which
 CC have chromosomal DNA encoding a binding site for p53 protein. Sequences
 CC AAX89356-366 represent oligonucleotides that are based on chromosomal
 CC binding sites for p53 protein.
 XX
 SQ Sequence 22 nt; 3 A; 7 C; 6 G; 15 T; 0 other;
 Alignment Scores:
 Pred. No.: 79.5 Length: 22
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-856-070-16 (1 5) x AAX89363 (1-22)
 QY 1 GluArgGluysGlu 5
 DB 22 GAAAGAGAAAGAA 8
 RESULT 5
 AAC89617/c
 ID AAC89617 standard; DNA: 25 BP.
 XX
 AC AAC89617;
 XX
 DT 08 MAR-2001 (first entry)
 DE S. cerevisiae YKR079C gene PCR primer A.
 XX
 KW Yeast, germination, proliferation, essential gene, antifungal agent;
 KW insecticide; herbicide; anti-proliferation drug; cancer; psoriasis;
 KW testolosis; YKR083C; YEF033C; YGP277C; YGP278W; YKR071C; YKR079C;
 KW YKR083C; PCR primer; ss.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO2000071161-A1.
 XX
 PD 30-NOV-2000
 XX
 PF 12-MAY-2000; 2000WO-US13017.
 XX
 PR 21-MAY-1999; 99US-0315794.
 PR 02-SEP-1999; 99US-0389341.
 XX
 PA (ROSE-) ROSETTA INPHARMATICS INC.
 XX
 PI Roberts CJ;
 XX
 DR WPI; 2001-025092/03.
 XX
 PT Identifying antifungal compounds which target yeast essential genes
 PT comprises use of novel Saccharomyces cerevisiae essential genes
 PT YEF033C, YGP277C, YGP278W, YKR071C, YKR079C or YKR083C
 XX
 PS Example 5; Fig 28; 127pp; English.
 XX
 CC The present invention provides methods of identifying antifungal agents
 CC using the coding and protein sequences of several yeast genes. These are
 CC essential for the germination and proliferation of Saccharomyces
 CC cerevisiae, and include YEF033C, YEF033C, YGP277C, YGP278W, YKR071C,
 CC YKR079C and YKR083C. The sequences can also be used to identify compounds
 CC for use as herbicides, insecticides and anti-proliferation drugs which
 CC can be used in the treatment of cancer, psoriasis and testolosis. This is
 CC because they can be used to identify plant, insect and human homologues
 CC of the yeast genes.
 XX
 SQ Sequence 25 nt; 4 A; 8 C; 1 G; 12 T; 0 other;

US-09-856-070-16 (1-5) x AAA56796 (1-37)

QY 1 GluArgGluLysGlu 5
ID AAA56792 standard; DNA; 37 EP.
DB 37 GAAAGAGAGAGAGAG 23
RESULT 8
AA56792/c
ID AAA56792 standard; DNA; 37 EP.
AC AAA56792;
XX 17-OCT-2000 (first entry)
XX Multiple triplex reporter forming probe MTRF9.
XX Multiple triplex reporter forming; MTRF; self-complexing;
KW nucleic acid detection; signal amplification system;
KW genetic hereditary testing; infectious disease; cancer;
KW initiator probe; ss.
XX Synthetic.
OS WO200029624-A2.
PN 25-MAY-2000.
XX 19-NOV-1999; 99WO-US27525.
XX 19-NOV-1998; 98US-0109082.
PR 27-JAN-1999; 99US-0117389.
PR 07-MAY-1999; 99US-0132976.
XX (CYGE) CYGENE INC.
PA Ramberg ER;
PI WPI: 2000-387827/33.
DE Multiple Triplex Receptor Forming (MTRF) self-complexing probe
PT composition useful for detection and analysis of nucleic acids,
PT comprises an initiator probe and at least two MTRF probes -
PS Disclosure: Page 76, 142pp, English.
XX The present sequence is the multiple triplex receptor forming
CC (MTRF) probe MTRF9. It is a component of a MTRF self-complexing probe
CC composition which may be used for detection and analysis of nucleic
CC acid sequences and for signal amplification. The composition comprises
CC at least 2 MTRF probes and an initiator probe. The MTRF probes
CC complex to the initiator probe to form triplex nucleic acid
CC structures, which together form the self-complexing probe. The MTRF
CC system may be used for direct RNA analysis and DNA diagnostic
CC analysis. It is useful for early and sensitive detection of
CC infectious disease and cancer and for genetic hereditary testing.
CC The system provides high sensitivity and specificity and is easy to
CC automate.
XX Sequence 37 BP; 0 A; 16 C; 0 G; 20 T; 1 other;

Alignment Scores:
Pred. No.: 137 Length: 37
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-070-16 (1-5) x AAA56792 (1-37)

QY 1 GluArgGluLysGlu 5
ID AAA56792 standard; DNA; 37 EP.
DB 37 GAAAGAGAGAGAGAG 23

DB 37 GAAAGAGAGAGAGAG 23

RESULT 9
AAH79199/c
ID AAH79199 standard; DNA; 41 BP.
XX AAH79199;
AC AAH79199;
XX 21-NOV-2001 (first entry)
XX Human receptor-related protein tyrosine phosphatase 11 probe 1.
DE Human, receptor-related protein tyrosine phosphatase 11; cytostatic;
XX virus; anti-inflammatory; anti-infectious; haemostatic;
KW malignant neoplasm; HIV; human immunodeficiency virus; infection;
KW immunological disease; developmental disorder; probe; ss.
XX Homo sapiens.
OS WO200166591-A1.
PN 13-SEP-2001.
PD 26-SEP-2001; 2001WO-CN0213.
PF 07-MAY-2000; 2000CN-011925.
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA Mao Y, Xie Y;
PI WPI: 2001-589931/66.
XX Human receptor-related protein tyrosine phosphatase 11 and encoded
PT polypeptide for diagnosis and treatment of malignant neoplasm,
PT haemopathy, HIV infection, immunological diseases and various
PT inflammations -
XX Example 6; Page 15, 36pp; Chinese.
XX The invention relates to human receptor-related protein tyrosine
CC phosphatase 11 and the encoding polynucleotide with cytostatic,
CC virucidal, immunomodulatory, anti-inflammatory and haemostatic activity.
CC The polypeptide and encoded polynucleotide are applicable in diagnosis
CC and treatment of malignant neoplasm, haemopathy, HIV infection,
CC immunological diseases, various inflammations and developmental
CC disorders. The present sequence is that of a human receptor-related
CC protein tyrosine phosphatase 11 probe, useful to the invention.
XX Sequence 41 BP, 0 A, 16 C, 5 G, 20 T, 0 other;

Alignment Scores:
Pred. No.: 153 Length: 41
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-070-16 (1-5) x AAH79199 (1-41)

QY 1 GluArgGluLysGlu 5
ID AAH79199 standard; DNA; 41 BP.
DB 34 GAAAGAGAGAGAGAG 20

RESULT 10
ABK40858/c
ID ABK40858 standard; DNA; 47 BP.
XX ABK40858;
XX 21-MAY-2002 (first entry)
XX

DE Human obesity-associated chromosome 3 biallelic marker #26.
 XX human; obesity associated biallelic marker, chromosome 3, obesity; ds;
 KW drug response; hypericaemia, digestive pathology; hypertension; cancer;
 KW hepatic function disorder, cardiovascular disease, hyperlipidaemia;
 KW insulin disorder; atheromatous disease; cardiac insufficiency.
 XX Homo sapiens.
 OS WO200206525-A2.
 PN 24-JAN-2002.
 PP 28-JUN-2001; 2001WO-IB01477.
 XX 18-JUL-2000; 2000US-219704P.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;
 PI WPI; 2002-155943/20.
 XX Set of novel map-related biallelic markers, preferably located on
 PT obesity disorder-associated chromosomal regions on chromosomes 3, 10
 PT and 19, useful, for e.g. detecting statistical correlations between
 PT marker allele and a phenotype.
 XX Claim 1; Page 214; 31pp; English.
 XX The invention relates to a set of novel map-related biallelic markers,
 CC preferably located on obesity disorder-associated chromosomal regions on
 CC chromosomes 3, 10 and 19. The markers are useful for genotyping or
 CC estimating the frequency of an allele in a population, for detecting an
 CC association between a genotype or haplotype and a phenotype, e.g. a
 CC disease involving drug responses, obesity or disorders related to
 CC obesity, such as hyperuricaemia, digestive pathology, hepatic function
 CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,
 CC insulin disorders, atheromatous disease and cardiac insufficiency. The
 CC markers are useful for detecting a statistical correlation between a
 CC biallelic marker allele and a phenotype and/or between a biallelic marker
 CC haplotype and a phenotype. This sequence represents a human
 CC obesity-associated biallelic marker located on chromosome 3
 XX Sequence 47 BP, 8 A, 13 C, 2 G, 23 T, 1 other,
 SO Alignment Scores:
 Pred. No.: 176 Length: 47
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-070-16 (1-5) x ABK40858 (1-47)
 QY 1 GluArgGluIysGlu 5
 ID 18 GAAAGAGAGAGAGAG 4
 AC AAA33591
 XX AAQ33591
 XX 02-FEB-1993 (first entry)
 DT DT
 DE Microsatellite sequence from clone AGLA285.
 XX PCR; selection, primers, OPTIPRM, breeding, cattle, parentage,
 KW genetic mapping; traits; amplification; ss.
 XX

OS Bos taurus.
 XX WO9213102-A.
 PN 06-AUG-1992.
 XX 15-JAN-1992; 92WO-050040.
 XX 15-JAN-1991; 91US-0642342.
 XX (GHNM-) GENMARK.
 PA Georges M, Massey JM;
 PI WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding
 PT Table 7, Page 165, 517pp, English.
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
 CC one out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (16)n > 9 microsatellites in the bovine genome is estimated at >100.
 CC 000 The sequence information for ca. 230 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci, or genes involved in the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAU33501-34437.
 XX Sequence 49 BP, 33 A, 9 C, 16 G, 6 U, 6 other;
 SO Alignment Scores:
 Pred. No.: 184 Length: 49
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-09-856-070-16 (1-5) x AAQ33591 (1-49)
 QY 1 GluArgGluIysGlu 5
 ID 24 CAGAGAGAGAGAGAG 38
 AC AAA76638
 XX AAA76638
 XX 16-NOV-2000 (first entry)
 DT DT
 DE Human clone c92539388 polymorphic site, SEQ ID NO:321.
 XX Human; single nucleotide polymorphism; SNP;
 KW detection; identification; gene therapy; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 PH variation replace (26,T)
 FT /*tag= a
 XX

PN WC2000029623-A2.
 XX 25-MAY-2000.
 XX 17-NOV-1999; 99WO-US27293.
 XX 17-NOV-1998; 98US-0109024.
 PR 16-NOV-1999; 99US-0109024.
 XX (CURA-) CURAGEN CORP.
 PA Shimketa RA, Leach MD;
 XX WPI: 2000-387826/33.
 XX Human nucleic acids containing single nucleotide polymorphisms, useful
 PT for treating a subject suffering, or at risk from a pathology due to
 PT the presence of a sequence polymorphism -
 XX
 PR Claim 1: Page 255; 543pp; English.
 XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
 CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
 CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
 CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
 CC consecutive pairs of nucleotides containing SNPs which result in changes
 CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
 CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
 CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
 CC in non-conservative changes. The SNPs in sequences 1187 to 1192
 CC (AAA77504-A77509) generate frameshift mutations. The invention also
 CC relates to a method of detecting a polymorphic site in a nucleic acid and
 CC a method of determining the relatedness of two nucleic acids. It also
 CC encompasses peptides containing polymorphic sites, antibodies raised
 CC against such peptides, and a method of detecting polymorphic
 CC proteins/peptides using the antibodies. The nucleic acids are useful for
 CC gene therapy of an individual having, suspected of having, or at risk of
 CC developing a pathological condition due to the presence of a sequence
 CC polymorphism. Such treatment would comprise administration of the
 CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
 CC peptides can also be used in the treatment of such individuals.
 XX
 SQ Sequence 51 BP; 20 A, 7 C, 15 G, 9 T, 0 other.

Alignment Scores:
 Pred. No. 192 Length: 51
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-070-16 (1-5) x AAA76638 (1-51)

QY 1 GluArgGluIysGlu 5
 |||||

DB 32 GAACGTCGAAAGGAA 46

RESULT 13
 AAA76639

ID AAA76639 standard; cDNA: 51 BP.

XX AAA76639;

XX 16-NOV-2000 (first entry)

DE Human clone c25304488 polymorphic site, SEQ ID NO:322.

XX Human: single nucleotide polymorphism; SNP;

XX detection; identification; gene therapy; ss.

OS Homo sapiens.

XX

PH Key Location/Qualifiers
 FT variation replace (26,C)
 FT /*tag- a

XX WC2000029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US27293.

XX 17-NOV-1998; 98US-0109024.

XX 16-NOV-1999; 99US-0109024.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach MD;

XX WPI: 2000-387826/33.

XX Human nucleic acids containing single nucleotide polymorphisms, useful
 PT for treating a subject suffering, or at risk from a pathology due to
 PT the presence of a sequence polymorphism -

XX Claim 1: Page 255; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
 CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
 CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
 CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
 CC consecutive pairs of nucleotides containing SNPs which result in changes
 CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
 CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
 CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
 CC in non-conservative changes. The SNPs in sequences 1187 to 1192
 CC (AAA77504-A77509) generate frameshift mutations. The invention also
 CC relates to a method of detecting a polymorphic site in a nucleic acid and
 CC a method of determining the relatedness of two nucleic acids. It also
 CC encompasses peptides containing polymorphic sites, antibodies raised
 CC against such peptides, and a method of detecting polymorphic
 CC proteins/peptides using the antibodies. The nucleic acids are useful for
 CC gene therapy of an individual having, suspected of having, or at risk of
 CC developing a pathological condition due to the presence of a sequence
 CC polymorphism. Such treatment would comprise administration of the
 CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
 CC peptides can also be used in the treatment of such individuals.

XX Sequence 51 BP; 20 A, 6 C, 15 G, 10 T, 0 other;

Alignment Scores:

Pred. No. 192 Length: 51
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-070-16 (1-5) x AAA76639 (1-51)

QY 1 GluArgGluIysGlu 5
 |||||

DB 32 GAACGTCGAAAGGAA 46

RESULT 14

AAQ33612

ID AAQ33612 standard; DNA: 58 BP.

XX AAQ33612;

XX 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone ACLA300.

XX PCR: selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.
 XX Bos taurus.
 XX W09213102-A.
 XX 06-AUG-1992.
 XX 15-JAN-1992; 92WO-US00340.
 XX 15-JAN-1991; 91US-0642342.
 XX (GENM) GENMARK.
 XX Georges M. Massey IM.
 XX WPI: 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding
 PT Table 7; Page 174; 517pp; English.
 XX The sequence is that of a bovine microsatellite sequence used by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50 clones cross hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (TAC)_n microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca 200 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program Optiprimer). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economically important loci, or genes involved in the determination of economically important traits esp. in cattle, to allow selective breeding.
 XX See also AAQ33501-34437
 XX Sequence 58 BP; 30 A; 0 C; 28 G; 0 U; 0 other;
 Alignment Scores:
 Pred. No.: 220 Length: 58
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14 Indels: 0
 DB: Gaps: 0
 US-09-856-070-16 (1-5) x AAQ33612 (1-58)
 QY 1 GluArgGluIysGlu 5
 Db 6 GAGAGAGAGAGAGAG 20
 W09213102 15
 ARN44740
 Id ARN44740 standard: DNA: 60 BP.
 XX
 XX ARN44740;
 XX 15 JUL 2002 (first entry)
 XX Human spliced transcript detection oligonucleotide SEQ ID NO:17488.
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX Homo sapiens.
 XX W0200210449-A2.
 XX

PD 07-FEB-2002.
 XX 20-JUL-2001; 2001WO-1H01903.
 XX 28-NOV-2000; 2000US-221607P.
 XX 02-MAY-2001; 2001US-28724P.
 XX (COMP-) COMPUGEN INC.
 XX Shoshan A. Wasserman A. Mintz E. Mintz L. Faigler S;
 XX WPI: 2002-257383/30.
 XX New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental specific genes -
 XX Example 1; SEQ ID 17488; 47pp; English.
 XX The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub)transcriptome, where the (sub)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which includes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology specific genes such as those genes only expressed in specific tissue under a specific pathological condition, to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ARN27253 to ARN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.
 XX N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pat_sequences.
 XX Sequence 60 BP; 36 A; 1 C; 22 G; 1 U; 0 other;
 Alignment Scores:
 Pred. No.: 228 Length: 60
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-070-16 (1-5) x ARN44740 (1-60)
 QY 1 GluArgGluIysGlu 5
 Db 14 GAGAGAGAGAGAGAA 28
 Search completed: January 16, 2003, 17:19:25
 Job time : 82.9821 secs